

SEQUENCE LISTING

<110> Pfizer Products Inc

<120> FUSION PROTEINS COMPRISING CARRIERS THAT CAN INDUCE A
DUAL IMMUNE RESPONSE

<130> PC10202A

<140>

<141>

<150> N/A

<151> 1999-02-17

<160> 46

<170> PatentIn Ver. 2.1

<210> 1

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 1

catggaacac tggctcttatg gtctgcgtcc ggg

33

<210> 2

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 2

catggaacac tggctcttatg gtctgcgtcc ggg

33

<210> 3

<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 3
gatctggaac actggtctta tggctgcgt ccgggc

36

<210> 4
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 4
gatcgcccg acgcagacca taagaccagt gttcca

36

<210> 5
<211> 76
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 5
gatccatgga gcactggtca tatggtctgc gtccgggtga acattggagc tacggtctac 60
gccccgggtc catggc 76

<210> 6
<211> 76
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 6

tcgagccatg gacccggggc gtagaccgta gctccaatgt tcacccggac gcagaccata 60
tgaccagtgc tccatg 76

<210> 7

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 7

ggggaacact ggtcttatgg cttacggccg ggagagcatt ggagttacgg cctccgtcca 60
ggttccatgg c 71

<210> 8

<211> 75

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 8

tcgagccatg gaacctggac ggaggccgta actccaatgc tctcccggcc gtaagccata 60
agaccagtgt tcccc 75

<210> 9

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 9
gatccagagc actgggtcata tgggtctgcgt ccgggtgaac attggagcta cggtctacgc 60
cccggggatc c 71

<210> 10
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 10
tcgaggatcc ccggggcgta gaccgtagct ccaatgttca ccgggacgca gaccatatga 60
ccagtgtct g 71

<210> 11
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 11
ggggaacact ggtcttatgg ctacggccg ggagagcatt ggagttacgg cctccgtcca 60
ggggatcc 68

<210> 12
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SYNTHETIC
OLIGONUCLEOTIDE COMPRISING GNRH CODING SEQUENCE
AND CLONING ENDS

<400> 12
tcgaggatcc cctggacgga ggccgtaact ccaatgtct cccggccgta agccataaga 60

ccagtgttcc cc

72

<210> 13
<211> 10
<212> PRT
<213> GNRH AMINO ACID SEQUENCE

<400> 13
Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
1 5 10

<210> 14
<211> 328
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: part of
plasmid p9897-R

<400> 14
acgccagggt tttcccagtc acgacgttgt aaaacgacgg ccagtgagcg cgcgtaatac 60
gactcactat agggcggaatt ggagctccac cgcggtggcg gccgctctag aactagtgga 120
tccagagcac tggatcatatg gtctgcgtcc gggatgaacat tggagctacg gtctacgcc 180
cggggaacac tggatcttatg gcttacggcc gggagagcat tggagttacg gcctccgtcc 240
aggttccatg ggctcgaggg ggggcccggg acccagcttt tgttcccttt agtgagggtt 300
aattgcgcgc ttggcgtaat atggtcat 328

<210> 15
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GnRH tetramer

<400> 15
Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly
1 5 10 15

Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His
20 25 30

Trp Ser Tyr Gly Leu Arg Pro Gly
35 40

5

EXPRESS MAIL NO. EL16282034US

<210> 16
<211> 1259
<212> DNA
<213> Bovine herpesvirus 1

<220>
<221> gene
<222> (1)..(1259)
<223> sequence encoding BHV-1 gD from clone
FlgD/Pots207(#79)

<400> 16
ccatggagggg gccgacattg gccgtgctgg gcgcgctgct cgcggttgcg gtaagcttgc 60
ctacaccgcg gccgcgggtg acggtatacg tcgaccgcgc ggcgtaaccg atgccgcgat 120
acaactacac tgaacgctgg cacactaccg ggcccatacc gtcgcccctc gcagacggcc 180
gcgagcagcc cgtcgagggtg cgctacgcga cgagcgcggc ggcggtgcgac atgctggcgc 240
tgatcgcaga cccgcagggtg gggcgcacgc tgtgggaagc ggtacgccgg cacgcgcgcg 300
cgtacaacgc caccgtcata tggtaacaaga tcgagagcgg gtgcgcccgg ccgctgtact 360
acatggagta caccgagtgc gagcccagga agcacttttg gtactgccgc taccgcacac 420
ccccgttttg ggacagcttc ctggcgggct tcgcctaccc cacggacgac gagctgggac 480
tgattatggc ggcgcccgcg cggctcgtcg agggccagta ccgacgcgcg ctgtacatcg 540
acggcacggg cgcctataca gatttcattg ttctcgtgcc ggccggggac tgctggttct 600
cgaaactcgg cgcggctcgc gggtaacact ttggcgcggtg cttcccggcc cgggattacg 660
agcaaaagaa ggttctgcgc ctgacgtatc tcacgcagta ctaccgcgag gaggcacaca 720
aggccatagt cgactactgg ttcattgcgc acggggggcg cgttcgcgcg tattttgagg 780
agtcgaaggc ctacgagccg ccgcctgccg ccgatggggg ttccccgcg ccaccggcg 840
acgacgaggc ccgcgaggat gaaggggaga ccgaggacgg ggcagccggg cgggagggca 900
acggcgggcc cccaggaccc gaaggcgacg gcgagagtca gaccccgaa gccaacggag 960
gcgcccaggc cgagccgaaa cccggcccca gcccgcagc cgaccgcccc gaaggctggc 1020
cgagcctcga agccatcacg cccccccgc ccgccccgc tacgcccgtc cgagctccgg 1080
acgctgtttc ggtttctggt ggtatcggtg tcgctgctgc tgctatcgtc tgcgttgctg 1140
ctgctgctgc tgggtgcttac ttcgtttata ttcgctcgtc tgggtgctgg ccgctgcgcg 1200
gtaaaccgaa aaaactgccg gctttcggtg acgttaacta cagtgcctcg ccgggttga 1259

<210> 17
<211> 418
<212> PRT
<213> Bovine herpesvirus 1

<220>
<221> PEPTIDE
<222> (1)..(418)
<223> BHV-1gD encoded by clone FlgD/Pots207nco(#79)

<400> 17

Met Glu Gly Pro Thr Leu Ala Val Leu Gly Ala Leu Leu Ala Val Ala
 1 5 10 15
 Val Ser Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro
 20 25 30
 Pro Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr
 35 40 45
 Thr Gly Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val
 50 55 60
 Glu Val Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu
 65 70 75 80
 Ile Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg
 85 90 95
 His Ala Arg Ala Tyr Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser
 100 105 110
 Gly Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro
 115 120 125
 Arg Lys His Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp
 130 135 140
 Ser Phe Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu
 145 150 155 160
 Ile Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala
 165 170 175
 Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu
 180 185 190
 Pro Ala Gly Asp Cys Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr
 195 200 205
 Thr Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val
 210 215 220
 Leu Arg Leu Thr Tyr Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys
 225 230 235 240
 Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro
 245 250 255

Tyr Phe Glu Glu Ser Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly
 260 265 270
 Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly
 275 280 285
 Glu Thr Glu Asp Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro
 290 295 300
 Gly Pro Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly
 305 310 315 320
 Ala Glu Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro
 325 330 335
 Glu Gly Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro
 340 345 350
 Ala Thr Pro Ala Arg Ala Pro Asp Ala Val Ser Val Ser Val Gly Ile
 355 360 365
 Gly Ile Ala Ala Ala Ala Ile Ala Cys Val Ala Ala Ala Ala Ala Gly
 370 375 380
 Ala Tyr Phe Val Tyr Ile Arg Arg Arg Gly Ala Gly Pro Leu Pro Arg
 385 390 395 400
 Lys Pro Lys Lys Leu Pro Ala Phe Gly Asn Val Asn Tyr Ser Ala Leu
 405 410 415
 Pro Gly

<210> 18
 <211> 1405
 <212> DNA
 <213> Bovine herpesvirus 1

<220>
 <221> gene
 <222> (1)..(1405)
 <223> BHV-1 gD from GenBank Accession No. M59846.

<400> 18
 gggccgcagc cccggctggg tatatatccc cgacgggcga ctagagatac actcgccccg 60
 cgcggtgct gcgagcgggc gaacatgcaa gggccgacat tggccgtgct gggcgcgctg 120
 ctcgccgttg cggtagactt gcctacaccc gcgccgcggg tgacggtata cgtcgacccg 180


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ccggcggtacc cgatgcgcgcg atacaactac actgaacgct ggcacactac cgggcccata 240
ccgtcgccct tcgcagacgcg ccgcgagcag cccgtcgagg tgcgctacgc gacgagcgcg 300
gcggcggtgcg acatgctggc gctgatcgca gaccgcgagg tggggcgcac gctgtgggaa 360
gcggtacgcc ggcacgcgcg cgcgtacaac gccacggtca tatggtacaa gatcgagagc 420
gggtgcgccc ggccgctgta ctacatggag tacaccgagt gcgagcccag gaagcacttt 480
gggtactgcc gctaccgcac acccccgttt tgggacagct tcctggcggg cttegcctac 540
cccacggacg acgagctggg actgattatg gcggcgcccg cgcggctcgt cgagggccag 600
taccgacgcg cgctgtacat cgacggcacg gtcgcctata cagatttcac ggtttcgctg 660
ccggccgggg actgctggtt ctcgaaactc ggcgcggtc gcgggtacac ctttggcgcg 720
tgcttcccgc cccgggatta cgagcaaaaag aaggttctgc gcctgacgta tctcacgcag 780
tactaccgcg aggaggcaca caaggccata gtcgactact ggttcatgcg ccacggggggc 840
gtcgttccgc cgtattttga ggagtcgaag ggctacgagc cgccgcctgc cgccgatggg 900
ggttccccgc cgccaccgcg cgacgacgag gcccgcgagg atgaagggga gaccgaggac 960
ggggcagccg ggccgggagg caacggcggc ccccaggac ccgaaggcga cggcgagagt 1020
cagacccccg aagccaacgc aggcgcgcg gcgcgagccga aaccgggcc cagccccgac 1080
gccgaccgcc ccgaaggctg gccgagcctc gaagccatca cgcaccccc gcccgcccc 1140
gctacgcccg cgcccccg caagcggtgc gtcagcgctc ggatcggcac tgcggctgcg 1200
gcgatcgctg cgtggtggcg cgccgcgcgc ggcgcgctact tcgtctatac gcgcggcgcg 1260
ggtgcgggtc cgtgcccag aaagccaaaa aagctgcccg ctttggcaa cgtcaactac 1320
agcgcgctgc ccgggtgagc ggcctaggcc ctccccgcac cgcccccttt gctcctagcc 1380
ccggctcctg ccgagccgcg cggggg                                     1405

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<210> 19

<211> 417

<212> PRT

<213> Bovine herpesvirus 1

<220>

<221> PEPTIDE

<222> (1)..(417)

<223> BHV-1 gD encoded by GenBank Accession No. M59846.

<400> 19

```

Met Gln Gly Pro Thr Leu Ala Val Leu Gly Ala Leu Leu Ala Val Ala
  1                   5                   10                   15

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```

Val Ser Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro
                   20                   25                   30

```

```

Pro Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr
                   35                   40                   45

```

```

Thr Gly Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val
                   50                   55                   60

```

```

Glu Val Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu
                   65                   70                   75                   80

```

Ile Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg
85 90 95

His Ala Arg Ala Tyr Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser
100 105 110

Gly Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro
115 120 125

Arg Lys His Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp
130 135 140

Ser Phe Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu
145 150 155 160

Ile Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala
165 170 175

Leu Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu
180 185 190

Pro Ala Gly Asp Cys Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr
195 200 205

Thr Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val
210 215 220

Leu Arg Leu Thr Tyr Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys
225 230 235 240

Ala Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro
245 250 255

Tyr Phe Glu Glu Ser Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly
260 265 270

Gly Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly
275 280 285

Glu Thr Glu Asp Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro
290 295 300

Gly Pro Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly
305 310 315 320

Ala Glu Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro
325 330 335

Glu Gly Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro
340 345 350

Ala Thr Pro Ala Ala Pro Asp Ala Val Pro Val Ser Val Gly Ile Gly
355 360 365

Ile Ala Ala Ala Ala Ile Ala Cys Val Ala Ala Ala Ala Gly Ala
370 375 380

Tyr Phe Val Tyr Thr Arg Arg Arg Gly Ala Gly Pro Leu Pro Arg Lys
385 390 395 400

Pro Lys Lys Leu Pro Ala Phe Gly Asn Val Asn Tyr Ser Ala Leu Pro
405 410 415

Gly

<210> 20

<211> 1218

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequence from
pQE-tmgD encoding a tmgD.

<400> 20

ctcgagaaat cataaaaaat ttatttgctt tgtgagcgga taacaattat aatagattca 60
attgtgagcg gataacaatt tcacacagaa ttcattaaag aggagaaatt aactatgaga 120
ggatctcacc atcaccatca ccatacggat ccgcatgccca tgagcttgcc tacaccgcgcg 180
ccgcgggtga cgggtatacgt cgaccgcgcg gcgtaccgca tgccgcgata caactacact 240
gaacgctggc aactaccgcg gccataccg tcgcccttcg cagacggccg cgagcagccc 300
gtcgaggtgc gctacgcgac gagcgcggcg gcgtgcgaca tgctggcgct gatcgagac 360
ccgcaggtgg ggcgcacgct gtgggaagcg gtacgccggc acgcgcgcgc gtacaacgcc 420
acggtcatat ggtacaagat cgagagcggg tcgcgccggc cgctgtacta catggagtac 480
accgagtgcg agcccaggaa gcactttggg tactgccgct accgcacacc cccgttttgg 540
gacagcttcc tggcgggctt cgcctacccc acggacgacg agctgggact gattatggcg 600
gcgcccgcgc ggctcgtcga gggccagtag cgacgcgcgc tgtacatcga cggcacgggc 660
gcctatacag atttcatggt ttcgctgccg gccggggact gctggttctc gaaactcggc 720
gcggctcgcg ggtacacctt tggcgcgtgc ttcccggccc gggattacga gaaaagaag 780
gttctgcgcc tgacgtatct cacgcagtag taccgcagg aggcacacaa ggccatagtc 840
gactactggt tcatgcgcca cgggggcgtc gttccgccgt attttgagga gtcgaagggc 900
tacgagccgc cgctgcgcgc cgatgggggt tccccgcgc caccggcgca cgacgaggcc 960
cgcgaggatg aaggggagac cgaggacggg gcagccgggc gggagggcaa cggcgccccc 1020
ccaggacccg aaggcgacgg cgagagtcag acccccgaag ccaacggagg cgccgagggc 1080

gagccgaaac cccgccccag ccccgacgcc gaccgccccg aaggctggcc gagcctcgaa 1140
gccatcacgc accccccgcc cgcgcccgct acgcccgtc gagctcggtg ccccggtcg 1200
acctgcagcc aagcttaa 1218

<210> 21
<211> 367
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: tmgD encoded
by pQE-tmgD.

<400> 21
Met Arg Gly Ser His His His His His His Thr Asp Pro His Ala Met
1 5 10 15
Ser Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro Pro
20 25 30
Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr Thr
35 40 45
Gly Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Glu
50 55 60
Val Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu Ile
65 70 75 80
Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg His
85 90 95
Ala Arg Ala Tyr Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser Gly
100 105 110
Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro Arg
115 120 125
Lys His Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser
130 135 140
Phe Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile
145 150 155 160
Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu
165 170 175

Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro
 180 185 190
 Ala Gly Asp Cys Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr
 195 200 205
 Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu
 210 215 220
 Arg Leu Thr Tyr Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala
 225 230 235 240
 Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr
 245 250 255
 Phe Glu Glu Ser Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly Gly
 260 265 270
 Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu
 275 280 285
 Thr Glu Asp Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly
 290 295 300
 Pro Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala
 305 310 315 320
 Glu Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro Glu
 325 330 335
 Gly Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala
 340 345 350
 Thr Pro Ala Arg Ala Arg Tyr Pro Gly Ser Thr Cys Ser Gln Ala
 355 360 365

<210> 22
 <211> 1360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: portion of
 pQE-GnRH:gD, including sequence encoding
 4GnRH-tmgD.

<400> 22

ctcgagaaat cataaaaaat ttatttgctt tgtgagcgga taacaattat aatagattca 60
attgtgagcg gataacaatt tcacacagaa ttcattaaag aggagaaatt aactatgaga 120
ggatctcacc atcaccatca ccatacggat ccgcatgccca tggatccaga gcaactggta 180
tatgggtctgc gtccgggtga acattggagc tacgggtctac gccccgggga acactgggtct 240
tatggcttac ggccgggaga gcattggagt tacggcctcc gtccaggttc catgagcttg 300
cctacacccg cgccgcgggt gacggtatac gtcgacccgc cggcgtagcc gatgcccga 360
tacaactaca ctgaacgctg gcacactacc gggcccatac cgtcgccctt cgcagacggc 420
cgcgagcagc ccgtcgaggt gcgctacgcg acgagcgcgg cggcggtgca catgctggcg 480
ctgatcgagc acccgaggtt ggggcgcacg ctgtgggaag cggtagcccg gcacgcgcgc 540
gcgtagaacg ccacggtcat atggtacaag atcgagagcg ggtgcgcccg gccgctgtac 600
tacatggagt acaccgagtg cgagcccagg aagcactttg ggtactgccg ctaccgcaca 660
cccccgtttt gggacagctt cctggcgggc ttcgcctacc ccacggacga cgagctggga 720
ctgattatgg cggcgcccgc gcggctcgtc gagggccagt accgacgcgc gctgtacatc 780
gacggcacgg tcgcctatac agatttcatg gtttcgctgc cggccgggga ctgctgggtc 840
tcgaaactcg gcgcggctcg cgggtacacc tttggcgcgt gcttcccggc ccgggattac 900
gagcaaaaaga aggttctgcg cctgacgtat ctcacgcagt actaccgca ggaggcacac 960
aaggccatag tcgactactg gttcatgcgc cacgggggcg tcgttccgcc gtattttgag 1020
gagtcgaagg gctacgagcc gccgcctgcc gccgatgggg gttccccgc gccaccgcgc 1080
gacgacgagg ccgcgagga tgaaggggag accgaggacg gggcagcccg gcgggagggc 1140
aacggcggcc cccagggacc cgaaggcgac ggcgagagtc agacccccga agccaacgga 1200
ggcgccgagg gcgagccgaa acccgcccc agccccgacg ccgaccgcc cgaaggctgg 1260
ccgagcctcg aagccatcac gcacccccg cccgccccg ctacgccgc tcgagctcgg 1320
taccggggt cgacctgcag ccaagcttaa ttagctgagc 1360

<210> 23

<211> 411

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 4GnRH-tmgD
encoded by pQE-GnRH:gD.

<400> 23

Met Arg Gly Ser His His His His His His Thr Asp Pro His Ala Met
1 5 10 15

Asp Pro Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser
20 25 30

Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
35 40 45

Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Ser Met Ser Leu Pro Thr
50 55 60

Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro Pro Ala Tyr Pro Met

65		70		75		80
Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr Thr Gly Pro Ile Pro						
	85		90		95	
Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Glu Val Arg Tyr Ala						
	100		105		110	
Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu Ile Ala Asp Pro Gln						
	115		120		125	
Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg His Ala Arg Ala Tyr						
	130		135		140	
Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser Gly Cys Ala Arg Pro						
	145		150		155	160
Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro Arg Lys His Phe Gly						
	165		170		175	
Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe Leu Ala Gly						
	180		185		190	
Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile Met Ala Ala Pro						
	195		200		205	
Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu Tyr Ile Asp Gly						
	210		215		220	
Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro Ala Gly Asp Cys						
	225		230		235	240
Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr Phe Gly Ala Cys						
	245		250		255	
Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg Leu Thr Tyr						
	260		265		270	
Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala Ile Val Asp Tyr						
	275		280		285	
Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr Phe Glu Glu Ser						
	290		295		300	
Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro						
	305		310		315	320
Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu Thr Glu Asp Gly						

325

330

335

Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro Glu Gly Asp
340 345 350

Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu Gly Glu Pro
355 360 365

Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro Glu Gly Trp Pro Ser
370 375 380

Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala Thr Pro Ala Arg
385 390 395 400

Ala Arg Tyr Pro Gly Ser Thr Cys Ser Gln Ala
405 410

<210> 24

<211> 1360

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: portion of
pQE-gD:GnRH, including sequence coding tmgD-4GnRH.

<400> 24

ctcgagaaat cataaaaaat ttatttgctt tgtgagcgga taacaattat aatagattca 60
attgtgagcg gataacaatt tcacacagaa ttcattaaag aggagaaatt aactatgaga 120
ggatctcacc atcaccatca ccatacggat ccgcatgccca tgagcttgcc tacacccgcg 180
ccgcgggtga cgggtatacgt cgacccgccg gcgtacccga tgccgcgata caactacact 240
gaaacgctggc aactaccgg gccataccg tcgcccttcg cagacggccg cgagcagccc 300
gtcgaggtgc gctacgcgac gagcgcggcg gcgtgcgaca tgctggcgct gatcgagac 360
ccgcaggtgg ggcgacgct gtgggaagcg gtacgccggc acgcgcgcgc gtacaacgcc 420
acggtcatat ggtacaagat cgagagcggg tgcgcccggc cgctgtacta catggagtac 480
accgagtgcg agcccaggaa gcactttggg tactgccgt accgcacacc cccgttttg 540
gacagcttcc tggcgggctt cgccatcccc acggacgacg agctgggact gattatggcg 600
gcgcccgcgc ggctcgtcga gggccagtag cgacgcgcgc tgtacatcga cggcacgggc 660
gcctatacag atttcatggt ttcgctgcgc gccggggact gctggttctc gaaactcggc 720
gcggctcgcg ggtacacctt tggcgcgtgc ttcccggccc gggattacga gcaaaagaag 780
gttctgcgcc tgacgtatct cagcgagtag taccgcgagg aggcacacaa ggccatagtc 840
gactactggt tcatgcgcca cgggggcgct gttccgccgt attttgagga gtcgaagggc 900
tacgagccgc cgctgcgcgc cgatgggggt tccccgcgc caccgcgca cgacgaggcc 960
cgcgaggatg aaggggagac cgaggacggg gcagccgggc gggagggcaa cggcggcccc 1020
ccaggacccg aaggcgacgg cgagagtcag acccccgaag ccaacggagg cgcgagggc 1080
gagccgaaac ccggccccag ccccgacgcc gaccgccccg aaggctggcc gagcctcgaa 1140
gccatcacgc accccccgcc cgccccgcgt acgcccgcgc gagctccaga gcactggtca 1200

tatgggtctgc gtccgggtga acattggagc tacgggtctac gccccgggga aactggtct 1260
 tatggcttac ggccgggaga gcattggagt tacggcctcc gtccaggttg aagcttaatt 1320
 agctgagctt ggactcctgt tgatagatcc agtaatgacc 1360

<210> 25
 <211> 398
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: tmgD-4GmRH
 encoded by pQE-gD:GnRH.

<400> 25
 Met Arg Gly Ser His His His His His His Thr Asp Pro His Ala Met
 1 5 10 15
 Ser Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro Pro
 20 25 30
 Ala Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr Thr
 35 40 45
 Gly Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Glu
 50 55 60
 Val Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu Ile
 65 70 75 80
 Ala Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg His
 85 90 95
 Ala Arg Ala Tyr Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser Gly
 100 105 110
 Cys Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro Arg
 115 120 125
 Lys His Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser
 130 135 140
 Phe Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile
 145 150 155 160
 Met Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu
 165 170 175

Tyr Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro
180 185 190

Ala Gly Asp Cys Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr
195 200 205

Phe Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu
210 215 220

Arg Leu Thr Tyr Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala
225 230 235 240

Ile Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr
245 250 255

Phe Glu Glu Ser Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly Gly
260 265 270

Ser Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu
275 280 285

Thr Glu Asp Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly
290 295 300

Pro Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala
305 310 315 320

Glu Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro Glu
325 330 335

Gly Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala
340 345 350

Thr Pro Ala Arg Ala Pro Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
355 360 365

Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly
370 375 380

Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
385 390 395

<210> 26

<211> 1441

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: portion of
pQE-GnRH:gD:GnRH, including encoding
4GnRH-tmgD-4GnRH

<400> 26

ctcgagaaat cataaaaaat ttatttgctt tgtgagcgga taacaattat aatagattca 60
attgtgagcg gataacaatt tcacacagaa ttcattaaag aggagaaatt aactatgaga 120
ggatctcacc atcaccatca ccatacggat ccgcatgcc aaggatccaga gcaactggtca 180
tatggctctg gtccgggtga acattggagc tacgggtctac gccccgggga acaactggtct 240
tatggcttac ggccgggaga gcattggagt tacggcctcc gtccagggtt catgagcttg 300
cctacaccgg cgccgggggt gacggtatac gtcgaccggc cggcgtagcc gatgccggca 360
tacaactaca ctgaacgctg gcacactacc gggcccatac cgtcgccctt cgcagacggc 420
cgcgagcagc ccgctgaggt gcgctacggc acgagcggc cggcgtagca catgctggcg 480
ctgatcgagc acccgaggt gggggcgacg ctgtgggaag cggtagcccg gcacggcgcg 540
gcgtacaacg ccacggtcat atgggtacaag atcgagagcg ggtgcggccg gccgctgtac 600
tacatggagt acaccgagtg cgagcccagg aagcactttg ggtactgccg ctaccgcaca 660
cccccgtttt gggacagctt cctggcgggc ttgcctacc ccacggacga cgagctggga 720
ctgattatgg cgccggccgc gcggctcgtc gagggccagt accgacggcg gctgtacatc 780
gacggcacgg tcgcctatac agatttcatg gtttcgctgc cggccgggga ctgctgggtc 840
tcgaaactcg gcgcggtcg cgggtacacc tttggcgctg gttcccgcc cggggattac 900
gagcaaaaaga aggttctgcg cctgacgtat ctcacgcagt actaccgca ggaggcacac 960
aaggccatag tcgactactg gttcatgcgc cacggggggc tcgttccgcc gtattttgag 1020
gagtcgaagg gctacgagcc gccgcctgcc gccgatgggg gttccccgc gccaccggcg 1080
gacgacgagg ccgcgagga tgaaggggag accgaggagc gggcagccgg gcgggagggc 1140
aacggcgggc ccccaggacc cgaaggcgac ggcgagagtc agaccccga agccaacgga 1200
ggcgccgagg gcgagccgaa acccgggccc agccccgac cgcacggccc cgaaggctgg 1260
ccgagcctcg aagccatcac gcaccccccg cccgcccccg ctacggccgc tcgagctcca 1320
gagcactggt catatggtct gcgtccgggt gaacattgga gctacggtct acgccccggg 1380
gaacactggt cttatggctt acggccggga gagcattgga gttacggcct ccgtccaggt 1440
t 1441

<210> 27

<211> 442

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
4GnRH-tmgD-4GnRH encoded by pQE-GnRH:gD:GnRH

<400> 27

Met Arg Gly Ser His His His His His His Thr Asp Pro His Ala Met
1 5 10 15
Asp Pro Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser
20 25 30

Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
 35 40 45
 Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Ser Met Ser Leu Pro Thr
 50 55 60
 Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro Pro Ala Tyr Pro Met
 65 70 75 80
 Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr Thr Gly Pro Ile Pro
 85 90 95
 Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Glu Val Arg Tyr Ala
 100 105 110
 Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu Ile Ala Asp Pro Gln
 115 120 125
 Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg His Ala Arg Ala Tyr
 130 135 140
 Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser Gly Cys Ala Arg Pro
 145 150 155 160
 Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro Arg Lys His Phe Gly
 165 170 175
 Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe Leu Ala Gly
 180 185 190
 Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile Met Ala Ala Pro
 195 200 205
 Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu Tyr Ile Asp Gly
 210 215 220
 Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro Ala Gly Asp Cys
 225 230 235 240
 Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr Phe Gly Ala Cys
 245 250 255
 Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg Leu Thr Tyr
 260 265 270
 Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala Ile Val Asp Tyr
 275 280 285

Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr Phe Glu Glu Ser
290 295 300

Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly Gly Ser Pro Ala Pro
305 310 315 320

Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu Thr Glu Asp Gly
325 330 335

Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro Glu Gly Asp
340 345 350

Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu Gly Glu Pro
355 360 365

Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro Glu Gly Trp Pro Ser
370 375 380

Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala Thr Pro Ala Arg
385 390 395 400

Ala Pro Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser
405 410 415

Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
420 425 430

Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
435 440

<210> 28

<211> 1079

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: portion of
pCMV-tgD, including sequence encoding a truncated
gD

<400> 28

gatatcatgc aggggccgac attggccgtg ctgggcgcgc tgctcgccgt tgcggtaagc 60
ttgcctacac ccgcgccgcg ggtgacggta tacgtcgacc cgccggcgta cccgatgccg 120
cgatacaact aactgaacg ctggcacact accgggcca taccgtcgcc cttcgcagac 180
ggccgcgagc agcccgtcga ggtgcgctac gcgacgagcg cggcggcggtg cgacatgctg 240
gcgctgatcg cagaccgcga ggtggggcgc acgctgtggg aagcggtagc ccggcacgcg 300

cgcgcggtaca acgccacggt catatggtac aagatcgaga gcgggtgcgc ccggccgctg 360
tactacatgg agtacaccga gtgcgagccc aggaagcact ttgggtactg ccgctaccgc 420
acacccccgt tttgggacag cttcctggcg ggcttcgcct accccacgga cgacgagctg 480
ggactgatta tggcgggcgcc cgcgcggtc gtcgagggcc agtaccgacg cgcgctgtac 540
atcgacggca cggtcgccta tacagatttc atggtttcgc tgccggccgg ggactgctgg 600
ttctcgaaac tcggcgcggc tcgcgggtac acctttggcg cgtgcttccc ggcccgggat 660
tacgagcaaa agaaggttct gcgcctgacg tatctcacgc agtactacc gcaggaggca 720
cacaaggcca tagtcgacta ctggttcacg cgccacgggg gcgtcgttcc gccgtatatt 780
gaggagtcga agggctacga gccgcgcct gccgccgatg ggggttcccc cgcgccaccc 840
ggcgacgacg agggccgcga ggatgaagg gagaccgagg acggggcagc cgggcgggag 900
ggcaacggcg gccccccagg acccgaaggc gacggcgaga gtcagacccc cgaagccaac 960
ggaggcgccg agggcgagcc gaaacccggc cccagccccg acgccgaccg ccccgaggct 1020
ggccgagcct cgaagccatc acgcaccccc cgcccgcccc cgctacgcc tgaggtacc 1079

<210> 29

<211> 353

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: truncated gD
encoded by pCMV-tgD

<400> 29

Met Gln Gly Pro Thr Leu Ala Val Leu Gly Ala Leu Leu Ala Val Ser
1 5 10 15

Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro Pro Ala
20 25 30

Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr Thr Gly
35 40 45

Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Glu Val
50 55 60

Arg Tyr Ala Thr Ser Ala Ala Cys Asp Met Leu Ala Leu Ile Ala
65 70 75 80

Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg His Ala
85 90 95

Arg Ala Tyr Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser Gly Cys
100 105 110

Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro Arg Lys
115 120 125

22

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His Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe
130 135 140

Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile Met
145 150 155 160

Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu Tyr
165 170 175

Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro Ala
180 185 190

Gly Asp Cys Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr Phe
195 200 205

Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg
210 215 220

Leu Thr Tyr Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala Ile
225 230 235 240

Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr Phe
245 250 255

Glu Glu Ser Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly Gly Ser
260 265 270

Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu Thr
275 280 285

Glu Asp Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro
290 295 300

Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu
305 310 315 320

Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro Glu Gly
325 330 335

Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala Thr
340 345 350

Pro

<210> 30

<211> 1241
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: portion of
pCMV-gD:GnRH, including sequence encoding a
tgD-4GnRH fusion protein

<400> 30

gcgggccgcaa gatatcatgc agggggccgac attggccgtg ctggggcgcgcg tgctcgccgt 60
tgcggttaagc ttgcctacac ccgcgccgcg ggtgacggtg tacgtcgacc cgccggcgta 120
cccgatgccg cgatacaact aactgaacg ctggcacact accggggcca taccgtcgcc 180
cttcgcagac ggccgcgagc agcccgctga ggtgcgctac gcgacgagcg cggcgggcgtg 240
cgacatgctg gcgctgatcg cagacccgca ggtggggcgcg acgctgtggg aagcggtacg 300
ccggcacgcg cgcgcgctaca acgccacggt catatggtac aagatcgaga gcgggtgcgc 360
ccggccgctg tactacatgg agtacaccga gtgcgagccc aggaagcact ttgggtactg 420
ccgctaccgc acacccccgt tttgggacag cttcctggcg ggcttcgcct accccacgga 480
cgacgagctg ggactgatta tggcgggcgcc cgcgcggtcg gtcgagggcc agtaccgacg 540
cgcgctgtac atcgacggca cggtcgccta tacagatttc atggtttcgc tgccggccgg 600
ggactgctgg ttctcgaaac tcggcgcgcg tcgcggggtac acctttggcg cgtgcttccc 660
ggcccgggat tacgagcaaa agaaggttct gcgcctgacg tatctcacgc agtactaccc 720
gcaggaggca cacaaggcca tagtcgacta ctggttcacg cgccacgggg gcgtcgttcc 780
gccgtatattt gaggagtcga agggctacga gccgccgcct gccgccgatg ggggttcccc 840
cgcgccaccc ggcgacgacg agggccgcga ggatgaaggg gagaccgagg acggggcagc 900
cgggcggggg ggcaacggcg gccccccagg acccgaaggc gacggcgaga gtcagacccc 960
cgaagccaac ggaggcgccg agggcgagcc gaaacccggc ccagccccg acgccgaccg 1020
ccccgaaggc tggccgagcc tcgaagccat cacgcacccc ccgcccggcc ccgctacgcc 1080
cgctcgagct ccagagcact ggtcatatgg tctgcgtccg ggtgaacatt ggagctacgg 1140
tctacgcccc ggggaacact ggtcttatgg cttacggccg ggagagcatt ggagttacgg 1200
cctccgtcca ggttgaagct gggatactag tgagcgggcg c 1241

<210> 31
<211> 397
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: tgD-4GnRH
fusion protein encoded by pCMV-gD:GnRH

<400> 31

Met Gln Gly Pro Thr Leu Ala Val Leu Gly Ala Leu Leu Ala Val Ser
1 5 10 15
Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro Pro Ala
20 25 30

Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr Thr Gly
 35 40 45
 Pro Ile Pro Ser Pro Phe Ala Asp Gly Arg Glu Gln Pro Val Glu Val
 50 55 60
 Arg Tyr Ala Thr Ser Ala Ala Ala Cys Asp Met Leu Ala Leu Ile Ala
 65 70 75 80
 Asp Pro Gln Val Gly Arg Thr Leu Trp Glu Ala Val Arg Arg His Ala
 85 90 95
 Arg Ala Tyr Asn Ala Thr Val Ile Trp Tyr Lys Ile Glu Ser Gly Cys
 100 105 110
 Ala Arg Pro Leu Tyr Tyr Met Glu Tyr Thr Glu Cys Glu Pro Arg Lys
 115 120 125
 His Phe Gly Tyr Cys Arg Tyr Arg Thr Pro Pro Phe Trp Asp Ser Phe
 130 135 140
 Leu Ala Gly Phe Ala Tyr Pro Thr Asp Asp Glu Leu Gly Leu Ile Met
 145 150 155 160
 Ala Ala Pro Ala Arg Leu Val Glu Gly Gln Tyr Arg Arg Ala Leu Tyr
 165 170 175
 Ile Asp Gly Thr Val Ala Tyr Thr Asp Phe Met Val Ser Leu Pro Ala
 180 185 190
 Gly Asp Cys Trp Phe Ser Lys Leu Gly Ala Ala Arg Gly Tyr Thr Phe
 195 200 205
 Gly Ala Cys Phe Pro Ala Arg Asp Tyr Glu Gln Lys Lys Val Leu Arg
 210 215 220
 Leu Thr Tyr Leu Thr Gln Tyr Tyr Pro Gln Glu Ala His Lys Ala Ile
 225 230 235 240
 Val Asp Tyr Trp Phe Met Arg His Gly Gly Val Val Pro Pro Tyr Phe
 245 250 255
 Glu Glu Ser Lys Gly Tyr Glu Pro Pro Pro Ala Ala Asp Gly Gly Ser
 260 265 270
 Pro Ala Pro Pro Gly Asp Asp Glu Ala Arg Glu Asp Glu Gly Glu Thr
 275 280 285

Glu Asp Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro
290 295 300

Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu
305 310 315 320

Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro Glu Gly
325 330 335

Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala Thr
340 345 350

Pro Ala Arg Ala Pro Glu His Trp Ser Tyr Gly Leu Arg Pro Gly Glu
355 360 365

His Trp Ser Tyr Gly Leu Arg Pro Gly Glu His Trp Ser Tyr Gly Leu
370 375 380

Arg Pro Gly Glu His Trp Ser Tyr Gly Leu Arg Pro Gly
385 390 395

<210> 32

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: sequence
encoding a GnRH tetramer

<400> 32

gagcactggt catatggtct gcgtccgggt gaacattgga gctacggtct acgccccggg 60
gaacactggt cttatggctt acggccggga gagcattgga gttacggcct ccgtccaggt 120

<210> 33

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: sequence
encoding a GnRH monomer

<400> 33

gagcactggt catatggtct gcgtccgggt

30

<210> 34
 <211> 1179
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: sequence
 encoding a 4GnRH-tmgD fusion protein

<400> 34
 gagcactggt catatggtct gcggtccgggt gaacattgga gctacggtct acgccccggg 60
 gaacactggt cttatggctt acggccggga gagcattgga gttacggcct ccgtccaggt 120
 tccatgagct tgcctacacc cgcgccgcgg gtgacggtat acgtcgaccc gccggcgtag 180
 ccgatgccgc gatacaacta cactgaacgc tggcacacta ccggggcccat accgtcgccc 240
 ttcgcagacg gccgcgagca gcccgtagag gtgcgctacg cgacgagcgc ggcgcggtgc 300
 gacatgctgg cgctgatcgc agaccgcgag gtggggcgca cgctgtggga agcggtacgc 360
 cggcacgcgc gcgcgtacaa cgccacgggtc atatggtaca agatcgagag cgggtgcgcc 420
 cggccgctgt actacatgga gtacaccgag tgcgagccca ggaagcactt tgggtactgc 480
 cgctaccgca ccccccggtt ttgggacagc ttcctggcgg gcttcgccta cccacggac 540
 gacgagctgg gactgattat ggcggcgccc gcgcggctcg tcgagggcca gtaccgacgc 600
 gcgctgtaca tcgacggcac ggtcgccat acagatttca tggtttcgct gccggccggg 660
 gactgctggt tctcgaaact cggcgcggtc cgcggtgaca cctttggcgc gtgcttccc 720
 gcccgggatt acgagcaaaa gaaggttctg cgctgacgt atctcacgca gtactacccg 780
 caggaggcac acaaggccat agtcgactac tggttcatgc gccacggggg cgctcgttccg 840
 ccgtattttg aggagtcgaa gggctacgag ccgcgcgctg ccgcgatgg gggttcccc 900
 gcgccacccg gcgacgacga ggccgcgag gatgaagggg agaccgagga cggggcagcc 960
 gggcgggagg gcaacggcgg cccccagga cccgaaggcg acggcgagag tcagaccccc 1020
 gaagccaacg gaggcgccga gggcgagccg aaaccgcggc ccagccccga cgccgaccgc 1080
 cccgaaggct ggccgagcct cgaagccatc acgcaccccc cgcccgcccc cgctacgccc 1140
 gctcgagctc ggtaccccg gtcgacctgc agccaagct 1179

<210> 35
 <211> 340
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: a truncated
 mature BHV-1 gD

<400> 35
 Leu Pro Thr Pro Ala Pro Arg Val Thr Val Tyr Val Asp Pro Pro Ala
 1 5 10 15

Tyr Pro Met Pro Arg Tyr Asn Tyr Thr Glu Arg Trp His Thr Thr Gly

30

Glu Asp Gly Ala Ala Gly Arg Glu Gly Asn Gly Gly Pro Pro Gly Pro

28

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275

280

285

Glu Gly Asp Gly Glu Ser Gln Thr Pro Glu Ala Asn Gly Gly Ala Glu
290 295 300

Gly Glu Pro Lys Pro Gly Pro Ser Pro Asp Ala Asp Arg Pro Glu Gly
305 310 315 320

Trp Pro Ser Leu Glu Ala Ile Thr His Pro Pro Pro Ala Pro Ala Thr
325 330 335

Pro Ala Arg Ala
340

<210> 36

<211> 1020

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: sequence
encoding a truncated mature BHV-1 gD

<400> 36

ttgcctacac ccgcgcgcgc ggtgacggta tacgtcgacc cgccggcgta cccgatgccg 60
cgatacaact aactgaacg ctggcacact accggggcca taccgtcgcc cttcgcagac 120
ggccgcgagc agcccgtcga ggtgcgctac gcgacgagcg cgccggcgctg cgacatgctg 180
gcgctgatcg cagaccgcga ggtggggcgc acgctgtggg aagcggtagc ccggcacgcg 240
cgcgcgtaga acgccacggt catatggtac aagatcgaga gcgggtgcgc ccggccgctg 300
tactacatgg agtacaccga gtgcgagccc aggaagcact ttgggtactg ccgctaccgc 360
acacccccgt tttgggacag cttcctggcg ggcttcgcct accccacgga cgacgagctg 420
ggactgatta tggcggcgcg ccgcgcggctc gtcgagggcc agtaccgacg cgcgctgtac 480
atcgacggca cggtcgccta tacagatttc atggtttcgc tgccggccgg ggactgctgg 540
ttctcgaaac tcggcgcggc tcgcgggtac acctttggcg cgtgcttccc ggcccgggat 600
tacgagcaaa agaaggttct gcgcctgacg tatctcacgc agtactacc gcaggaggca 660
cacaaggcca tagtcgacta ctggttcacg cgccacgggg gcgtcggtcc gccgtatttt 720
gaggagtcga agggctacga gccgcgcgct gccgcgcgatg ggggttccc ccgcgccacc 780
ggcgacgacg agggccgcga ggatgaagg gagaccgag acggggcagc cgggccccgag 840
ggcaacggcg gccccccagg acccgaagg gacggcgaga gtcagacccc cgaagccaac 900
ggaggcgccg agggcgagcc gaaaccggc ccagccccg acgcccagcg ccccgaggc 960
tggccgagcc tcgaagccat cagcaccacc ccgcccgcgc ccgctacgcc cgctcgagct 1020

<210> 37

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6XHIS leader

<400> 37

Met Arg Gly Ser His His His His His His Thr Asp Pro His Ala
1 5 10 15

<210> 38

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: sequence
encoding 6XHIS leader

<400> 38

atgagaggat ctcacccatca ccatcaccat acggatccgc atgcc 45

<210> 39

<211> 1017

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: open reading
frame for the 6XHIS leader, truncated mature gD,
and GnRH tetramer encoded by bac-gD:GnRH

<400> 39

atgagcttgc ctacaccgc gccgcgggtg acggtatacg tcgaccgcgc ggcgtaccgc 60
atgccgcgat acaactacac tgaacgctgg cacactaccg ggccatacc gtcgcccttc 120
gcagacggcc gcgagcagcc cgtcgagggtg cgctacgcga cgagcgcggc ggcgtgcgac 180
atgctggcgc tgatcgaga cccgcagggtg gggcgcacgc tgtgggaagc ggtacgcggg 240
cacgcgcgcg cgtacaacgc caccggtcata tgggtacaaga tcgagagcgg gtgcgcccgg 300
ccgctgtact acatggagta caccgagtgc gagcccagga agcactttgg gtactgccgc 360
taccgcacac ccccgttttg ggacagcttc ctggcgggct tcgcctaccc caccgacgac 420
gagctggggac tgattatggc ggcgcccgcg cggctcgtcg agggccagta ccgacgcgcg 480
ctgtacatcg acggcacggt cgcctataca gatttcatgg ttctcgtgcc ggccggggac 540
tgctggttct cgaaactcgg cgcggctcgc ggggtacacct ttggcgcgtg cttcccggcc 600
cgggattacg agcaaaagaa ggttctgcgc ctgacgtatc tcacgcagta ctaccgcgag 660
gaggcacaca aggccatagt cgactactgg ttcatgcgcc acggggggcgt cgttccgcgcg 720
tattttgagg agtcgaaggg ctacgagccg ccgcctgccg ccgatggggg ttccccgcgcg 780
ccaccgcggc acgacgaggc ccgcgaggat gaaggggaga ccgaggacgg ggcagccggg 840
cgggaggggca acggcgggcc cccaggaccc gaaggcgacg gcgagagtca gacccccgaa 900

gccaacggag ggcgcgaggg cgagccgaaa cccggcccca gccccgacgc cgaccgcccc 960
gaaggctggc cgagcctcga agccatcacg cccccccgc cgcccccg taogccc 1017

<210> 40
<211> 1272
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sequence
encoding a 4GnRH-tmgD-4GnRH fusion protein

<400> 40
gagcactggt catatggtct gcgctccgggt gaacattgga gctacggtct acgccccggg 60
gaacactggt cttatggctt acggccggga gagcattgga gttacggcct ccgtccaggt 120
tccatgagct tgcctacacc cgcgcgcggg gtgacggtat acgtcgaccc gcggcggtac 180
ccgatgccgc gatacaacta cactgaacgc tggcacacta ccggggcccat accgtcgccc 240
ttcgcagacg gccgcgagca gcccgtcgag gtgcgctacg cgacgagcgc ggcgggcggtgc 300
gacatgctgg cgctgatcgc agaccgcag gtggggcgca cgctgtggga agcggtacgc 360
cggcacgcgc gcgcgtacaa cgccacgggc atatggtaca agatcgagag cgggtgcgcc 420
cggccgctgt actacatgga gtacaccgag tgcgagccca ggaagcactt tgggtactgc 480
cgctaccgca ccccccggt ttgggacagc ttcctggcgg gcttcgccta ccccacggac 540
gacgagctgg gactgattat ggcgggcgccc gcgcggctcg tcgagggcca gtaccgacgc 600
gcgctgtaca tcgacggcac ggctgcctat acagatttca tggtttcgct gcggggccggg 660
gactgctggt tctcgaaact cggcgcggtc cgcggttaca cctttggcgc gtgcttcccc 720
gcccgggatt acgagcaaaa gaagggtctg cgcctgacgt atctcacgca gtactacccg 780
caggaggcac acaaggccat agtcgactac tggttcatgc gccacggggg cgtcgttccg 840
ccgtattttg aggagtcgaa gggctacgag ccgcccgcctg ccgccgatgg gggttcccc 900
gcgccacccg gcgacgacga ggcccgcgag gatgaagggg agaccgagga cggggcagcc 960
gggcggggagg gcaacggcgg cccccagga cccgaaggcg acggcgagag tcagaccccc 1020
gaagccaacg gaggcgcgca gggcgagccg aaacccggcc ccagccccga cgccgacgc 1080
cccgaaggct ggccgagcct cgaagccatc acgcaccccc cgcccgcccc cgctacgccc 1140
gtcgcgagtc cagagcactg gtcatatggt ctgcgtccgg gtgaacattg gagctacggt 1200
ctacgccccg gggaacactg gtcttatggc ttacggccgg gagagcattg gagttacggc 1260
ctccgtccag gt 1272

<210> 41
<211> 1144
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: sequence
encoding a tmgD-4GnRH fusion protein

<400> 41

cttgcctaca cccgcgcgcg ggggtgacggt atacgtcgac ccgcccggcgt acccgatgcc 60
 gcgataacaac tacactgaac gctggcacac taccggggccc ataccgtcgc ccttcgcaga 120
 cggccgcgag cagcccgtcg aggtgcgcta cgcgacgagc gcggcggcgt gcgacatgct 180
 ggcgctgata gcagaccgcg aggtggggcg cacgctgtgg gaagcgggtac gccggcacgc 240
 gcgcgcgtac aacgccacgg tcatatggta caagatcgag agcgggtgcg cccggcgcgt 300
 gtactacatg gagtacaccg agtgcgagcc caggaagcac tttgggtact gccgctaccg 360
 cacacccccg ttttgggaca gcttctctggc gggcttcgcc taccacacgg acgacgagct 420
 gggactgatt atggcggcgc ccgcgcggct cgtcgagggc cagtaccgac gcgcgctgta 480
 catcgacggc acggtcgctt atacagattt catggtttcg ctgccggccg gggactgctg 540
 gttctcgaaa ctccggcgcg ctccggggta cacctttggc gcgtgcttcc cggcccggga 600
 ttacgagcaa aagaagggtt tgcgcctgac gtatctcacg cagtactacc cgcaggaggc 660
 acacaaggcc atagtcgact actggttcat gcgccacggg ggcgctcgtt ccgcgtatatt 720
 tgaggagtcg aagggtacg agccgcgcgc tgccgcgcgt ggggggttcc ccgcgccacc 780
 cggcgacgac gaggcccgcg aggatgaagg ggagaccgag gacggggcag ccgggcggga 840
 gggcaacggc ggccccccag gaccgaagg cgacggcgag agtcagacc ccgaagccaa 900
 cggaggcgcc gagggcgagc cgaaaccgg cccagcccc gacgccgacc gcccgaagg 960
 ctggccgagc ctcaagcca tcaagcacc cccgcccgc cccgctacgc ccgctcgagc 1020
 tccagagcac tggatcatat gtctgcgtcc gggatgaacat tggagctacg gtctacgccc 1080
 cggggaacac tggctcttat gcttacggcc gggagagcat tggagttacg gcctccgtcc 1140
 aggt 1144

<210> 42

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer P14-S1

<400> 42

ggagctccag agcactggtc ata

23

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer
P14-A138

<400> 43

aaagcttcaa cctggacgga ggcc

24

<210> 44

<211> 215

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 44

Met Lys Lys Ala Val Leu Ala Ala Val Leu Gly Gly Ala Leu Leu Ala
1 5 10 15

Gly Ser Ala Met Ala His Gln Ala Gly Asp Val Ile Phe Arg Ala Gly
20 25 30

Ala Ile Gly Val Ile Ala Asn Ser Ser Ser Asp Tyr Gln Thr Gly Ala
35 40 45

Asp Val Asn Leu Asp Val Asn Asn Asn Ile Gln Leu Gly Leu Thr Gly
50 55 60

Thr Tyr Met Leu Ser Asp Asn Leu Gly Leu Glu Leu Leu Ala Ala Thr
65 70 75 80

Pro Phe Ser His Lys Ile Thr Gly Lys Leu Gly Ala Thr Asp Leu Gly
85 90 95

Glu Val Ala Lys Val Lys His Leu Pro Pro Ser Leu Tyr Leu Gln Tyr
100 105 110

Tyr Phe Phe Asp Ser Asn Ala Thr Val Arg Pro Tyr Val Gly Ala Gly
115 120 125

Leu Asn Tyr Thr Arg Phe Phe Ser Ala Glu Ser Leu Lys Pro Gln Leu
130 135 140

Val Gln Asn Leu Arg Val Lys Lys His Ser Val Ala Pro Ile Ala Asn
145 150 155 160

Leu Gly Val Asp Val Lys Leu Thr Asp Asn Leu Ser Phe Asn Ala Ala
165 170 175

Ala Trp Tyr Thr Arg Ile Lys Thr Thr Ala Asp Tyr Asp Val Pro Gly
180 185 190

Leu Gly His Val Ser Thr Pro Ile Thr Leu Asp Pro Val Val Leu Phe
195 200 205

Ser Gly Ile Ser Tyr Lys Phe
210 215

<210> 45
 <211> 364
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 45

Met	Lys	Lys	Ser	Leu	Val	Ala	Leu	Thr	Val	Leu	Ser	Ala	Ala	Ala	Val
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Ala	Gln	Ala	Ala	Pro	Gln	Gln	Asn	Thr	Phe	Tyr	Ala	Gly	Ala	Lys	Ala
			20					25					30		
Gly	Trp	Ala	Ser	Phe	His	Asp	Gly	Ile	Glu	Gln	Leu	Asp	Ser	Ala	Lys
		35						40					45		
Asn	Thr	Asp	Arg	Gly	Thr	Lys	Tyr	Gly	Ile	Asn	Arg	Asn	Ser	Val	Thr
		50					55					60			
Tyr	Gly	Val	Phe	Gly	Gly	Tyr	Gln	Ile	Leu	Asn	Gln	Asp	Lys	Leu	Gly
	65					70					75				80
Leu	Ala	Ala	Glu	Leu	Gly	Tyr	Asp	Tyr	Phe	Gly	Arg	Val	Arg	Gly	Ser
				85					90					95	
Glu	Lys	Pro	Asn	Gly	Lys	Ala	Asp	Lys	Lys	Thr	Phe	Arg	His	Ala	Ala
			100					105					110		
His	Gly	Ala	Thr	Ile	Ala	Leu	Lys	Pro	Ser	Tyr	Glu	Val	Leu	Pro	Asp
		115						120				125			
Leu	Asp	Val	Tyr	Gly	Lys	Val	Gly	Ile	Ala	Leu	Val	Asn	Asn	Thr	Tyr
	130						135					140			
Lys	Thr	Phe	Asn	Ala	Ala	Gln	Glu	Lys	Val	Lys	Thr	Arg	Arg	Phe	Gln
	145				150					155					160
Ser	Ser	Leu	Ile	Leu	Gly	Ala	Gly	Val	Glu	Tyr	Ala	Ile	Leu	Pro	Glu
				165					170					175	
Leu	Ala	Ala	Arg	Val	Glu	Tyr	Gln	Trp	Leu	Asn	Asn	Ala	Gly	Lys	Ala
			180					185					190		
Ser	Tyr	Ser	Thr	Leu	Asn	Arg	Met	Gly	Ala	Thr	Asp	Tyr	Arg	Ser	Asp
		195					200					205			
Ile	Ser	Ser	Val	Ser	Ala	Gly	Leu	Ser	Tyr	Arg	Phe	Gly	Gln	Gly	Ala
	210					215					220				

Val Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser
225 230 235 240

Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala
245 250 255

Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu
260 265 270

Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys
275 280 285

Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala
290 295 300

Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val
305 310 315 320

Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val
325 330 335

Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val
340 345 350

Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met
355 360

<210> 46

<211> 369

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 46

Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
1 5 10 15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
20 25 30

Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
35 40 45

Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
50 55 60

Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
65 70 75 80

35

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Asn Phe Gly Leu Ala Thr Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val
85 90 95

Arg Gly Asn Asp Gly Glu Phe Arg Ala Met Lys His Ser Ala His Gly
100 105 110

Leu Asn Phe Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
115 120 125

Val Tyr Gly Lys Val Gly Val Ala Val Val Arg Asn Asp Tyr Lys Ser
130 135 140

Tyr Gly Ala Glu Asn Thr Asn Glu Pro Thr Glu Lys Phe His Lys Leu
145 150 155 160

Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
165 170 175

Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
180 185 190

Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
195 200 205

Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
210 215 220

Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
225 230 235 240

Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
245 250 255

Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
260 265 270

Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
275 280 285

Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
290 295 300

Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
305 310 315 320

Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
325 330 335

Thr Cys Asp Lys Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
340 345 350

Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
355 360 365

Met

005720 02050560